What is claimed is:

1. A genetically modified coryneform bacterium, wherein the cdsA gene thereof, which codes for phosphatidate cytidylyl transferase, is amplified.

2. The genetically modified coryneform bacterium as claimed in claim 1, wherein the starting bacterium (wild type) is selected from the group *Corynebacterium glutamicum* (ATCC13032), Corynebacterium acetoglutamicum (ATCC15806), Corynebacterium acetoacidophilum (ATCC13870), Corynebacterium thermoaminogenes (FERM BP-1539), Corynebacterium melassecola (ATCC17965), Brevibacterium flavum (ATCC14067), Brevibacterium lactofermentum (ATCC13869) and Brevibacterium divaricatum (ATCC14020), or is selected from the group Corynebacterium glutamicum FERM-P 1709, Brevibacterium flavum FERM-P 1708, Brevibacterium lactofermentum FERM-P 1712, Corynebacterium glutamicum FERM-P 6463, Corynebacterium glutamicum FERM-P 6464 and Corynebacterium glutamicum DSM5715.

3. The genetically modified coryneform bacterium as claimed in claim 1, wherein the cdsA gene is amplified by overexpressing the gene.

4. The genetically modified coryneform bacterium as claimed in claim 3, wherein the cdsA gene is over-expressed by increasing the copy number of the gene, by selecting a strong promoter or a regulation region upstream from the reading frame, by mutating the promoter, the regulation region or the ribosome-binding site, by incorporating a suitable expression cassette upstream from the structural gene or by incorporating inducible promoters, by extending the lifetime of the corresponding mRNA, by reducing

degradation of the expressed proteins, or by combining two or more of these possibilities.

5. The genetically modified coryneform bacterium as claimed in claim 1, wherein the strain is transformed with a plasmid vector and the plasmid vector bears the nucleotide sequence which codes for the cdsA gene.

6. The genetically modified coryneform bacterium as claimed in claim 1, wherein said bacterium corresponds genotypically to the strain *Corynebacterium glutamicum* DSM 13252.

7. An isolated polynucleotide from coryneform bacteria containing a polynucleotide sequence selected from the group consisting of:

a) a polynucleotide which is at least 70% homologous to a polynucleotide which codes for a polypeptide which comprises or consists of the amino acid sequence of SEQ ID no. 2,

b) a polynucleotide which codes for a polypeptide which comprises an amino acid sequence which is at least 70% homologous to the amino acid sequence of SEQ ID no. 2,

c) a polynucleotide which is complementary to the polynucleotides of a) or b) and

d) a polynucleotide containing at least 15 successive nucleotides of the polynucleotide sequence of a), b) or c).

8. The polynucleotide as claimed in claim 7, wherein the polynucleotide is a recombinant DNA replicable in coryneform bacteria.

9. The polynucleotide as claimed in claim 7, wherein the polynucleotide is an RNA.

10. The polynucleotide as claimed in claim 7, wherein the DNA, which is capable of replication, comprises:

(i) the nucleotide sequence shown in SEQ ID no. 1, or

(ii) at least one sequence which corresponds to the sequence (i) within the degeneration range of the genetic code, or

(iii) at least one sequence which hybridizes with the complementary sequence to sequence (i) or (ii) and optionally

(iv) functionally neutral mutations in (i) which give rise to homologous amino acids.

11. The polynucleotide sequence as claimed in claim 10, which codes for a polypeptide which comprises the amino acid sequence SEQ ID no. 2.

12. A method for the fermentative production of L-amino acids, wherein, the following step is performed:

a) fermenting L-amino acid producing coryneform bacteria in which at least the cdsA gene or nucleotide sequences coding therefor is/are amplified.

13. The method according to claim 12; wherein the cdsA gene or nucleotide sequences which code for it is amplified by being over-expressed.

14. The method according to claim 12, further comprising:

b) accumulating the L-amino acid in the medium or in the cells of the bacteria.

15. The method according to claim 14, further comprising:

c) isolating the L-amino acid.

16. The method as claimed in claim 12, wherein a genetically modified coryneform bacterium, wherein the cdsA gene, which codes for cyclopropane-mycolic acid synthase, is amplified, is employed.

17. The method as claimed in claim 12, wherein, additional genes, which code for a protein of the biosynthetic pathway of the desired L-amino acid, are amplified in the bacteria.

18. The method as claimed in claim 12, wherein, metabolic pathways which reduce the formation of the desired amino acid are at least partially suppressed in the bacteria.

19. The method as claimed in claim 12, wherein, the amino acid produced is L-lysine.

20. The method as claimed in claim 12, wherein, bacteria are fermented for the production of lysine in which simultaneously one or more of the genes selected from the group consisting of:

a) the dapA gene which codes for dihydropicolinate synthase,

b) the dapE gene which codes for succinyldiamino pimelate desuccinylase,

c) the lysC gene which codes for a feed back resistant aspartate kinase,

d) the tpi gene which codes for triosephosphate isomerase,

e) the gap gene which codes for glyceraldehyde 3-phosphate dehydrogenase,

f) the pgk gene which codes for 3-phosphoglycerate

kinase,

g) the pyc gene which codes for pyruvate carboxylase,

h) the mqo gene which codes for malate:quinone oxidoreductase, and

i) the lysE gene which codes for lysine export,

is/are simultaneously amplified.

21. The method as claimed in claim 20, wherein said one or more genes is or are overexpressed at the same time they are fermented.

22. The method as claimed claim 12, wherein, bacteria are fermented for the production of L-lysine in which one or more genes selected from the group consisting of

a) the pck gene which codes for phosphoenolpyruvate carboxykinase,

b) pgi gene which codes for glucose 6-phosphate isomerase, and

c) the poxB gene which codes for pyruvate oxidase

is/are simultaneously attenuated.

23. A primer which comprises a polynucleotide sequence as claimed in claim 7 or parts thereof, and can produce DNA of genes which code for phosphatidate cytidylyl transferase by the polymerase chain reaction.

24. A hybridization probe which comprises a polynucleotide sequence as claimed in claim 7 and can isolate cDNA or genes which exhibit elevated homology with the sequence of the cdsA gene